Cluster	Cluster p-value	OTUs	Total	pos75	pos50	neg50	neg75	Phylum	Species	Similarity (%)
1	**$5.29e^{-10}$**	**207**	45	3	29	12	1	Firmicutes	*Faecalibacterium prausnitzii*	96.7
		5	38	4	21	12	1	Firmicutes	*Ruminococcus bromii*	99.8
		144	36	2	30	4	0	Firmicutes	*Faecalibacterium prausnitzii*	98.9
		18	33	0	13	16	3	Firmicutes	*Clostridium hylemonae*	98.5
		129	32	1	30	1	0	Firmicutes	*Ruminococcus schinkii*	96.7
		239	30	2	23	5	0	Bacteroidetes	*Bacteroides plebeius*	100
		6	30	2	22	4	1	Firmicutes	*Faecalibacterium prausnitzii*	98.8
		1	29	1	21	6	0	Bacteroidetes	*Bacteroides plebeius*	100
		45	29	4	22	2	0	Bacteroidetes	*Bacteroides massiliensis*	100
		152	28	0	24	4	0	Firmicutes	*Faecalibacterium prausnitzii*	89
		210	28	0	22	6	0	Firmicutes	*Ruminococcus bromii*	94.5
		171	26	0	22	4	0	Firmicutes	*Coprococcus catus*	95.3
		175	26	0	23	3	0	Bacteroidetes	*Bacteroides dorei*	95.3
		260	26	1	22	3	0	Bacteroidetes	*Bacteroides massiliensis*	99.6
		312	25	1	23	1	0	Bacteroidetes	*Bacteroides nordii*	99.7
		112	23	0	16	7	0	Firmicutes	*Faecalibacterium prausnitzii*	100
		146	23	0	20	3	0	Firmicutes	*Clostridium viride*	92.7
		315	20	0	19	1	0	Bacteroidetes	*Bacteroides massiliensis*	100
		286	19	0	17	2	0	Bacteroidetes	*Bacteroides massiliensis*	100
		134	18	0	15	3	0	Bacteroidetes	*Bacteroides nordii*	99.4
		195	18	0	17	1	0	Firmicutes	*Faecalibacterium prausnitzii*	98.8
		244	18	0	17	1	0	Firmicutes	*Faecalibacterium prausnitzii*	91.6
		59	18	0	11	7	0	Firmicutes	*Faecalibacterium prausnitzii*	98.8
		246	17	0	14	3	0	Firmicutes	*Blautia wexlerae*	93.9
		309	17	0	16	1	0	Firmicutes	*Ruminococcus bromii*	94.2
		69	17	0	10	7	0	Firmicutes	*Blautia glucerasea*	100
		250	16	0	6	10	0	Firmicutes	*Staphylococcus warneri*	100
		281	16	0	7	8	0	Firmicutes	*Clostridium hylemonae*	99.2
		323	16	0	15	1	0	Firmicutes	*Clostridium populeti*	97.5
		229	15	0	15	0	0	Firmicutes	*Ruminococcus torques*	97.6
		317	15	2	9	4	0	Firmicutes	*Ruminococcus gnavus*	99.8
		34	14	1	11	2	0	Firmicutes	*Ruminococcus lactaris*	96.4

		0	13	2	6	5	0	Firmicutes	*Ruminococcus gnavus*	100
		117	11	0	4	6	0	Bacteroidetes	*Parabacteroides merdae*	100
		237	11	0	3	8	0	Bacteroidetes	*Bacteroides coprocola*	99.8
		325	11	2	7	2	0	Firmicutes	*Ruminococcus gnavus*	100
		31	8	0	4	4	0	Proteobacteria	*Escherichia/Shigella flexneri*	99.8
		125	7	0	3	4	0	Bacteroidetes	*Barnesiella intestinihominis*	99
		65	7	0	6	1	0	Firmicutes	*Oscillibacter valericigenes*	94.5
		80	7	0	4	3	0	Firmicutes	*Eubacterium ramulus*	99.8
		296	6	0	4	2	0	Firmicutes	*Roseburia intestinalis*	99.7
		49	6	0	4	2	0	Firmicutes	*Roseburia inulinivorans*	99.6
		54	5	0	5	0	0	Firmicutes	*Clostridium orbiscindens*	95.9
		132	4	0	3	1	0	Firmicutes	*Ruminococcus callidus*	99.5
		99	4	0	3	1	0	Firmicutes	*Clostridium asparagiforme*	95.6
		158	2	0	1	1	0	Firmicutes	*Megamonas funiformis*	99.7
		43	2	0	1	1	0	Firmicutes	*Desulfotomaculum guttoideum*	97.3
		61	2	0	2	0	0	Firmicutes	*Faecalibacterium prausnitzii*	98.8
		166	1	0	1	0	0	Firmicutes	*Blautia luti*	98.6
		187	1	0	0	1	0	Firmicutes	*Ruminococcus lactaris*	96.4
		225	1	0	0	1	0	NA	*Insolitispirillum peregrinum*	82.5
		267	1	0	0	1	0	Bacteroidetes	*Bacteroides thetaiotaomicron*	90.1
		33	1	0	1	0	0	Bacteroidetes	*Alistipes onderdonkii*	97.1
2	**$1.26e^{-07}$**	**24**	26	1	16	8	0	Firmicutes	*Dorea formicigenerans*	100
		53	26	3	15	8	0	Proteobacteria	*Sutterella wadsworthensis*	100
		7	25	2	13	9	0	Bacteroidetes	*Bacteroides uniformis*	100
		98	23	3	12	6	0	Firmicutes	*Anaerostipes butyraticus*	97.6
		204	22	4	14	4	0	Bacteroidetes	*Bacteroides dorei*	98.4
		12	21	3	12	6	0	Firmicutes	*Dorea longicatena*	100
		36	21	0	6	15	0	Actinobacteria	*Bifidobacterium longum*	98.8
		177	20	2	14	4	0	Bacteroidetes	*Bacteroides dorei*	98.6
		241	20	0	16	4	0	Firmicutes	*Desulfotomaculum guttoideum*	97.7
		162	19	0	8	10	0	Bacteroidetes	*Bacteroides chinchillae*	99.5
		29	19	3	14	2	0	Bacteroidetes	*Parabacteroides distasonis*	98.3
		101	17	3	11	3	0	Bacteroidetes	*Bacteroides dorei*	99

		115	16	0	6	9	0	Bacteroidetes	*Bacteroides chinchillae*	100
		153	16	1	12	3	0	Firmicutes	*Clostridium bolteae*	95.3
		14	13	0	8	5	0	Bacteroidetes	*Bacteroides dorei*	98.6
		16	12	1	11	0	0	Firmicutes	*Ruminococcus torques*	100
		41	12	2	4	6	0	Firmicutes	*Desulfotomaculum guttoideum*	95.9
		126	11	0	10	1	0	Firmicutes	*Clostridium glycyrrhizinilyticum*	97.5
		288	11	0	10	1	0	Bacteroidetes	*Bacteroides dorei*	98.8
		155	10	0	9	0	0	Firmicutes	*Desulfotomaculum guttoideum*	96.8
		176	9	0	5	4	0	Proteobacteria	*Acinetobacter johnsonii*	99
		243	8	0	3	5	0	Proteobacteria	*Pseudomonas flavescens*	100
		304	8	0	5	3	0	Firmicutes	*Dorea longicatena*	100
		10	7	0	4	3	0	Firmicutes	*Clostridium nexile*	99.8
		270	7	0	7	0	0	Bacteroidetes	*Bacteroides dorei*	98.8
		259	5	0	5	0	0	Firmicutes	*Clostridium hylemonae*	97.1
		89	5	0	3	2	0	Actinobacteria	*Bifidobacterium adolescentis*	100
		93	4	0	3	1	0	Bacteroidetes	*Bacteroides acidifaciens*	95.9
		120	3	0	2	1	0	Proteobacteria	*Acinetobacter lwoffii*	100
		188	3	0	0	3	0	Firmicutes	*Anaerostipes caccae*	99.8
		245	3	0	2	1	0	Firmicutes	*Anoxybacillus rupiensis*	100
		258	3	0	3	0	0	Firmicutes	*Desulfotomaculum guttoideum*	96.9
		305	3	0	1	2	0	Bacteroidetes	*Sphingobacterium multivorum*	99.7
		86	3	0	3	0	0	Firmicutes	*Clostridium lactatifermentans*	93.5
		247	1	0	0	1	0	Firmicutes	*Lactobacillus delbrueckii*	100
3	**$5.86e^{-05}$**	**2**	24	1	19	4	0	Firmicutes	*Eubacterium rectale*	99.7
		199	18	0	12	6	0	Firmicutes	*Ruminococcus schinkii*	96.6
		151	17	1	9	7	0	Firmicutes	*Ruminococcus obeum*	100
		25	16	1	5	10	0	Fusobacteria	*Fusobacterium mortiferum*	98.6
		138	14	1	9	4	0	Bacteroidetes	*Alistipes shahii*	99.8
		19	13	0	7	6	0	Firmicutes	*Ruminococcus albus*	95.7
		131	12	0	7	5	0	Firmicutes	*Roseburia faecis*	99.7
		30	12	0	11	1	0	Firmicutes	*Clostridium orbiscindens*	100
		9	12	1	8	2	1	Firmicutes	*Blautia wexlerae*	99.8
		336	11	0	10	1	0	Firmicutes	*Clostridium orbiscindens*	99.8

		38	11	0	10	1	0	Firmicutes	*Clostridium bolteae*	99.5
		4	9	1	5	3	0	Bacteroidetes	*Bacteroides fragilis*	98.6
		116	8	0	7	1	0	Firmicutes	*Clostridium populeti*	94.5
		87	8	0	3	4	1	Firmicutes	*Clostridium lituseburense*	98
		106	7	0	6	1	0	Firmicutes	*Eubacterium desmolans*	98.2
		142	6	0	3	3	0	Firmicutes	*Granulicatella elegans*	100
		159	6	0	1	5	0	Firmicutes	*Alicyclobacillus pohliae*	99
		3	6	0	3	3	0	Bacteroidetes	*Bacteroides stercoris*	99
		71	6	0	6	0	0	Actinobacteria	*Eggerthella lenta*	99.6
		77	6	0	5	1	0	Firmicutes	*Dialister invisus*	100
		274	5	0	2	3	0	Bacteroidetes	*Bacteroides fragilis*	99.2
		255	4	0	2	2	0	Firmicutes	*Clostridium disporicum*	99.7
		51	4	0	3	1	0	Firmicutes	*Cellulosilyticum ruminicola*	92.6
		73	3	0	3	0	0	Bacteroidetes	*Bacteroides eggerthii*	99.5
		79	3	0	3	0	0	Actinobacteria	*Collinsella intestinalis*	99.5
		107	2	0	0	2	0	Proteobacteria	*Paracoccus yeei*	99.5
		191	2	0	1	1	0	Firmicutes	*Butyricicoccus pullicaecorum*	99.6
		203	2	0	1	1	0	Firmicutes	*Lactococcus lactis*	100
		303	1	0	0	1	0	Firmicutes	*Acetanaerobacterium elongatum*	92.9
		84	1	0	0	1	0	Bacteroidetes	*Odoribacter splanchnicus*	99.3
4	**$2.47e^{-06}$**	**20**	17	1	15	1	0	Firmicutes	*Gemmiger formicilis*	99.8
		48	16	1	14	1	0	Bacteroidetes	*Prevotella amnii*	84.5
		104	14	0	11	3	0	Firmicutes	*Clostridium orbiscindens*	90.8
		105	14	0	13	1	0	Firmicutes	*Dialister succinatiphilus*	98.7
		22	14	0	12	1	0	Firmicutes	*Clostridium aldenense*	96.4
		127	11	0	7	4	0	Bacteroidetes	*Bacteroides cellulosilyticus*	99.5
		161	11	2	9	0	0	Firmicutes	*Gemmiger formicilis*	100
		289	11	0	5	6	0	Firmicutes	*Clostridium saccharolyticum*	96.4
		39	11	0	8	3	0	Bacteroidetes	*Prevotella copri*	99.3
		240	9	0	9	0	0	Firmicutes	*Coprococcus eutactus*	95.4
		81	9	0	8	1	0	Actinobacteria	*Slackia piriformis*	90.4
		92	9	0	9	0	0	Firmicutes	*Coprococcus catus*	100
		157	8	0	8	0	0	Firmicutes	*Eubacterium eligens*	99.8

		301	8	0	2	6	0	Firmicutes	*Ruminococcus schinkii*	96.8
		47	8	0	8	0	0	Firmicutes	*Clostridium lactatifermentans*	95.2
		156	7	0	6	1	0	Proteobacteria	*Sutterella stercoricanis*	99.6
		291	5	0	5	0	0	NA	*Rhodospirillum rubrum*	87.7
		90	5	0	5	0	0	Proteobacteria	*Sutterella stercoricanis*	99
		249	4	0	3	0	0	Firmicutes	*Allisonella histaminiformans*	98.1
		37	4	0	3	1	0	Firmicutes	*Eubacterium hallii*	99.7
		44	4	0	2	2	0	Firmicutes	*Gemmiger formicilis*	97.6
		220	3	0	3	0	0	Proteobacteria	*Klebsiella pneumoniae*	100
		242	3	0	3	0	0	Firmicutes	*Lactobacillus taiwanensis*	100
		110	1	0	1	0	0	Firmicutes	*Mogibacterium pumilum*	92.3
		50	1	0	1	0	0	Firmicutes	*Lactobacillus rogosae*	99.8
		55	1	0	1	0	0	Proteobacteria	*Methylobacterium adhaesivum*	98.9
		63	1	0	1	0	0	Actinobacteria	*Collinsella aerofaciens*	99
		70	1	0	1	0	0	Firmicutes	*Sporobacter termitidis*	94.1
		83	1	0	1	0	0	NA	*Desulfotomaculum carboxydivorans*	86.7
		96	1	0	0	1	0	Firmicutes	*Gemmiger formicilis*	93.8
5	**$1.91e^{-4}$**	**60**	18	0	12	6	0	Firmicutes	*Clostridium ramosum*	99.8
		76	18	0	15	3	0	Proteobacteria	*Mesorhizobium australicum*	98.8
		91	12	0	11	1	0	Deinococcus-Thermus	*Thermus scotoductus*	99.5
		58	10	1	9	0	0	Proteobacteria	*Undibacterium oligocarboniphilum*	100
		139	9	0	8	1	0	Bacteroidetes	*Prevotella enoeca*	83.3
		224	8	0	8	0	0	Proteobacteria	*Bradyrhizobium yuanmingense*	99.5
		23	8	0	6	2	0	Firmicutes	*Streptococcus salivarius*	100
		108	7	0	7	0	0	Proteobacteria	*Pelomonas saccharophila*	99
		11	7	0	6	1	0	Firmicutes	*Thermanaeromonas toyohensis*	85.9
		227	7	0	6	1	0	Bacteroidetes	*Sediminibacterium salmoneum*	96
		28	7	1	5	1	0	Firmicutes	*Streptococcus mitis*	100
		46	7	0	5	2	0	Firmicutes	*Blautia hansenii*	99.8
		68	7	1	5	1	0	Proteobacteria	*Sphingomonas melonis*	99.8
		64	6	1	4	1	0	Firmicutes	*Gemella haemolysans*	99.8
		124	5	0	4	0	0	Firmicutes	*Granulicatella adiacens*	100
		264	5	0	5	0	0	Actinobacteria	*Actinomyces odontolyticus*	100

		123	4	0	0	3	0	Firmicutes	*Clostridium hylemonae*	97.5
		143	4	0	3	1	0	Bacteroidetes	*Lishizhenia tianjinensis*	86.9
		154	4	0	3	1	0	Proteobacteria	*Ralstonia insidiosa*	99.7
		205	4	0	3	1	0	Proteobacteria	*Comamonas aquatica*	98.7
		178	3	0	2	1	0	Actinobacteria	*Atopobium rimae*	100
		163	2	0	2	0	0	Firmicutes	*Streptococcus sinensis*	98.8
		57	2	0	2	0	0	Firmicutes	*Clostridium perfringens*	100
		74	2	0	2	0	0	Firmicutes	*Clostridium leptum*	95.2
		130	1	0	1	0	0	Proteobacteria	*Brevundimonas vesicularis*	100
		226	1	0	1	0	0	Bacteroidetes	*Sediminibacterium salmoneum*	98.1
ND	**ND**	**67**	26	3	15	8	0	Bacteroidetes	*Bacteroides caccae*	99.8
ND	**ND**	**230**	23	0	14	8	0	Bacteroidetes	*Bacteroides xylanisolvens*	99.8
ND	**ND**	**56**	20	1	14	5	0	Bacteroidetes	*Bacteroides nordii*	99.7
ND	**ND**	**21**	17	0	12	5	0	Bacteroidetes	*Bacteroides caccae*	100
ND	**ND**	**32**	15	2	12	1	0	Bacteroidetes	*Bacteroides thetaiotaomicron*	100
ND	**ND**	**327**	15	1	11	3	0	Bacteroidetes	*Bacteroides nordii*	99.5
ND	**ND**	**13**	14	1	11	2	0	Firmicutes	*Clostridium bolteae*	100
ND	**ND**	**223**	14	0	7	7	0	Actinobacteria	*Collinsella aerofaciens*	100
ND	**ND**	**8**	13	0	10	3	0	Firmicutes	*Blautia glucerasea*	98.8
ND	**ND**	**208**	12	0	10	2	0	Bacteroidetes	*Butyricimonas virosa*	98.3
ND	**ND**	**94**	10	0	10	0	0	Firmicutes	*Clostridium scindens*	100
ND	**ND**	**82**	8	0	7	1	0	Firmicutes	*Blautia hansenii*	100
ND	**ND**	**97**	8	0	7	1	0	Proteobacteria	*Bilophila wadsworthia*	99.7
ND	**ND**	**145**	5	0	5	0	0	Firmicutes	*Clostridium aldenense*	98
ND	**ND**	**169**	3	0	3	0	0	Firmicutes	*Ruminococcus obeum*	99.8
ND	**ND**	**277**	3	0	1	2	0	NA	*Bacteroides plebeius*	90.7
ND	**ND**	**251**	2	0	1	1	0	Actinobacteria	*Bifidobacterium breve*	100
ND	**ND**	**307**	1	0	1	0	0	Firmicutes	*Veillonella parvula*	99.8

Supp. Table 4: OTU correlation network composition deduced from patients in remission 6 months after ICR

Cluster: Identity of the cluster; OTUs: identity of the Operational Taxonomic Unit specific of each cluster; Total: total number of significant correlations between the identified OTU and other OTUs from the cluster; pos75: number of significant positive correlations (R≥0.75) between the identified OTU and other OTUs from the cluster; pos50: number of significant positive correlations (R≥0.50) between the identified OTU and other OTUs from the cluster; neg50: number of significant negative correlations (R≤-0.5) between the identified OTU and other OTUs from

the cluster; Similarity: similarity percentage between the OTU and the first relative species. No significant negative correlation with $R \leq -0.75$ was observed.